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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/995,225

DATE: 01/08/2002  
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7 <110> APPLICANT: Chen, Ruoping  
 10 Chu, Zhi Liang  
 13 Dang, Huong T.  
 16 Lowitz, Kevin P.  
 19 Pride, Cameron  
 25 <120> TITLE OF INVENTION: Endogenous And Non-Endogenous Versions of Human G Protein-  
 Coupled Receptors  
 26  
 32 <130> FILE REFERENCE: AREN-0308  
 C--> 38 <140> CURRENT APPLICATION NUMBER: US/09/995,225  
 C--> 38 <141> CURRENT FILING DATE: 2001-11-26  
 38 <150> PRIOR APPLICATION NUMBER: 09/170,496  
 41 <151> PRIOR FILING DATE: 1998-10-13  
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 65 <150> PRIOR APPLICATION NUMBER: 60/255,366  
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 86 <151> PRIOR FILING DATE: 2001-04-06  
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 140 <151> PRIOR FILING DATE: 2001-07-31  
 146 <160> NUMBER OF SEQ ID NOS: 67  
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 190 ggcctgtgct acaacgccct gctggtgctg gccaacctac acagcaaggc cagcatgacc 180  
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206 gccctgctga gcctcgacca ctacatcgag cgtgcactgc cgcggaccta catggccagc 420
210 gtgtacaaca cgcggcacgt gtgcggcttc gtgtggggtg gcgcgctgct gaccagcttc 480
214 tctcgtctgc tcttctacat ctgcagccat gtgtccaccc gcgcgctaga gtgcgccaag 540
218 atgcagaacg cagaagctgc cgacgccacg ctggtgttca tcggctacgt ggtgccagca 600
222 ctggccaccc tctacgcgct ggtgctactc tcccgcgtcc gcagggagga cacgcccctg 660
226 gaccgggaca cgggccggct ggagccctcg gcacacaggc tgctggtggc caccgtgtgc 720
230 acgcagtttg ggctctggac gccacactat ctgatcctgc tggggcacac ggtcatcatc 780
234 tcgcgaggga agcccgtaga cgcacactac ctggggctac tgcactttgt gaaggatttc 840
238 tccaaactcc tggccttctc cagcagcttt gtgacaccac ttctctaccg ctacatgaac 900
242 cagagcttcc ccagcaagct ccaacggctg atgaaaaagc tgccctgcgg ggaccggcac 960
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288 20 25 30
294 Gly Leu Val Val Gly Val Pro Val Gly Leu Cys Tyr Asn Ala Leu Leu
296 35 40 45
302 Val Leu Ala Asn Leu His Ser Lys Ala Ser Met Thr Met Pro Asp Val
304 50 55 60
310 Tyr Phe Val Asn Met Ala Val Ala Gly Leu Val Leu Ser Ala Leu Ala
312 65 70 75 80
318 Pro Val His Leu Leu Gly Pro Pro Ser Ser Arg Trp Ala Leu Trp Ser
320 85 90 95
326 Val Gly Gly Glu Val His Val Ala Leu Gln Ile Pro Phe Asn Val Ser
328 100 105 110
334 Ser Leu Val Ala Met Tyr Ser Thr Ala Leu Leu Ser Leu Asp His Tyr
336 115 120 125
342 Ile Glu Arg Ala Leu Pro Arg Thr Tyr Met Ala Ser Val Tyr Asn Thr
344 130 135 140
350 Arg His Val Cys Gly Phe Val Trp Gly Gly Ala Leu Leu Thr Ser Phe
352 145 150 155 160
358 Ser Ser Leu Leu Phe Tyr Ile Cys Ser His Val Ser Thr Arg Ala Leu
360 165 170 175
366 Glu Cys Ala Lys Met Gln Asn Ala Glu Ala Ala Asp Ala Thr Leu Val
368 180 185 190
374 Phe Ile Gly Tyr Val Val Pro Ala Leu Ala Thr Leu Tyr Ala Leu Val
376 195 200 205
382 Leu Leu Ser Arg Val Arg Arg Glu Asp Thr Pro Leu Asp Arg Asp Thr
384 210 215 220
390 Gly Arg Leu Glu Pro Ser Ala His Arg Leu Leu Val Ala Thr Val Cys

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398 Thr Gln Phe Gly Leu Trp Thr Pro His Tyr Leu Ile Leu Leu Gly His
400          245          250          255
406 Thr Val Ile Ile Ser Arg Gly Lys Pro Val Asp Ala His Tyr Leu Gly
408          260          265          270
414 Leu Leu His Phe Val Lys Asp Phe Ser Lys Leu Leu Ala Phe Ser Ser
416          275          280          285
422 Ser Phe Val Thr Pro Leu Leu Tyr Arg Tyr Met Asn Gln Ser Phe Pro
424          290          295          300
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432 305          310          315          320
438 Cys Ser Pro Asp His Met Gly Val Gln Gln Val Leu Ala
440          325          330
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471 ctccctggtga aaatgaacac ccggtcagtg accaccatgg cggtcattaa cttggtggtg 180
475 gtccacagcg tttttctgct gacagtgcc tttogcttga cctacctcat caagaagact 240
479 tggatgtttg ggctgccctt ctgcaaattt gtgagtgcc tgcctgcacat ccacatgtac 300
483 ctacagttcc tattctatgt ggtgatcctg gtcaccagat acctcatctt cttcaagtgc 360
487 aaagacaaag tggaattcta cagaaaactg catgctgtgg ctgccagtgc tggcatgtgg 420
491 acgctggtga ttgtcattgt ggtacccttg gttgtctccc ggtatggaat ccatgaggaa 480
495 tacaatgagg agcactgttt taaatttcac aaagagcttg cttacacata tgtgaaaatc 540
499 atcaactata tgatagtcac ttttgcata gccgttgctg tgattctgtt ggtcttcagg 600
503 gtcttcatca ttatgttgat ggtgcagaag ctacgccact cttactatc ccaccaggag 660
507 ttctgggctc agctgaaaaa cctatttttt ataggggtca tccttgtttg tttccttccc 720
511 taccagttct ttaggatcta ttacttgaat gttgtgacgc attccaatgc ctgtaacagc 780
515 aaggttgcat ttataacga aatcttcttg agtgtaacag caattagctg ctatgatttg 840
519 cttctctttg tctttggggg aagccattgg tttaagcaaa agataattgg cttatggaat 900
523 tgtgttttgt gccgttag
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532 <211> LENGTH: 305
535 <212> TYPE: PRT
538 <213> ORGANISM: Homo sapiens
544 <400> SEQUENCE: 4
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558          20          25          30
564 Val Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg
566          35          40          45
572 Ser Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val
574          50          55          60
580 Phe Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr
582 65          70          75          80

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596 Ile His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr
598      100      105      110
604 Arg Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg
606      115      120      125
612 Lys Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile
614      130      135      140
620 Val Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly Ile His Glu Glu
622 145      150      155      160
628 Tyr Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr
630      165      170      175
636 Tyr Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val
638      180      185      190
644 Ala Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val
646      195      200      205
652 Gln Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln
654      210      215      220
660 Leu Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro
662 225      230      235      240
668 Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn
670      245      250      255
676 Ala Cys Asn Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val
678      260      265      270
684 Thr Ala Ile Ser Cys Tyr Asp Leu Leu Leu Phe Val Phe Gly Gly Ser
686      275      280      285
692 His Trp Phe Lys Gln Lys Ile Ile Gly Leu Trp Asn Cys Val Leu Cys
694      290      295      300
700 Arg
702 305

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708 &lt;210&gt; SEQ ID NO: 5

711 &lt;211&gt; LENGTH: 1125

714 &lt;212&gt; TYPE: DNA

717 &lt;213&gt; ORGANISM: Artificial Sequence

723 &lt;220&gt; FEATURE:

726 &lt;223&gt; OTHER INFORMATION: Novel Sequence

730 &lt;400&gt; SEQUENCE: 5

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740 cccacgccc acgtcagcgg gctgagccag gagtttgaaa gccactggcc agagatcgca      180
744 gagaggtccc cgtgtgtggc tggcgtcatc cctgtcatct actacagtgt cctgctgggc      240
748 ttggggctgc ctgtcagcct cctgaccgca gtggccctgg cgcgccttgc caccaggacc      300
752 aggaggecct cctactacta ccttctggcg ctcacagcct cggatatcat catccaggtg      360
756 gtcacgtgtg tcgcgggctt cctcctgcag ggagcagtgc tggcccgcga ggtgccccag      420
760 gctgtggtgc gcacggccaa catcctggag tttgtgcca accacgcctc agtctggatc      480
764 gccatcctgc tcacggttga ccgctacact gccctgtgcc accccctgca ccatcggggc      540
768 gcctcgtccc caggccggac ccgcccggcc attgctgctg tcttgagtgc tgccctgttg      600
772 accggcatcc ccttctactg gtggctggac atgtggagag acaccgactc acccagaaca      660
776 ctggacgagg tcctcaagtg ggctcactgt ctcactgtct atttcatccc ttgtggcgtg      720

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780 ttctgtggtca ccaactcggc catcatccac cggctacgga ggaggggccc gagtgggctg      780
784 cagccccggg tgggcaagag cacagccatc ctctgggca tcaccacact gttcaccctc      840
788 ctgtgggccc cccgggtctt cgatcatgctc taccacatgt acgtggcccc tgtccaccgg      900
792 gactggaggg tccacctggc cttggatgtg gccaatatgg tggccatgct ccacacggca      960
796 gccaaacttcg gcctctactg ctttgtcagc aagactttcc gggccactgt ccgacaggtc     1020
800 atccacgatg cctacctgcc ctgcactttg gcatcacagc cagagggcat ggcggcgaag     1080
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825 <220> FEATURE:
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852 Gly Gln Pro Arg Val Thr Leu Leu Pro Thr Pro Asn Val Ser Gly Leu
854 35 40 45
860 Ser Gln Glu Phe Glu Ser His Trp Pro Glu Ile Ala Glu Arg Ser Pro
862 50 55 60
868 Cys Val Ala Gly Val Ile Pro Val Ile Tyr Tyr Ser Val Leu Leu Gly
870 65 70 75 80
876 Leu Gly Leu Pro Val Ser Leu Leu Thr Ala Val Ala Leu Ala Arg Leu
878 85 90 95
884 Ala Thr Arg Thr Arg Arg Pro Ser Tyr Tyr Tyr Leu Leu Ala Leu Thr
886 100 105 110
892 Ala Ser Asp Ile Ile Ile Gln Val Val Ile Val Phe Ala Gly Phe Leu
894 115 120 125
900 Leu Gln Gly Ala Val Leu Ala Arg Gln Val Pro Gln Ala Val Val Arg
902 130 135 140
908 Thr Ala Asn Ile Leu Glu Phe Ala Ala Asn His Ala Ser Val Trp Ile
910 145 150 155 160
916 Ala Ile Leu Leu Thr Val Asp Arg Tyr Thr Ala Leu Cys His Pro Leu
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924 His His Arg Ala Ala Ser Ser Pro Gly Arg Thr Arg Arg Ala Ile Ala
926 180 185 190
932 Ala Val Leu Ser Ala Ala Leu Leu Thr Gly Ile Pro Phe Tyr Trp Trp
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940 Leu Asp Met Trp Arg Asp Thr Asp Ser Pro Arg Thr Leu Asp Glu Val
942 210 215 220
948 Leu Lys Trp Ala His Cys Leu Thr Val Tyr Phe Ile Pro Cys Gly Val
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956 Phe Leu Val Thr Asn Ser Ala Ile Ile His Arg Leu Arg Arg Arg Gly
958 245 250 255
964 Arg Ser Gly Leu Gln Pro Arg Val Gly Lys Ser Thr Ala Ile Leu Leu
966 260 265 270
972 Gly Ile Thr Thr Leu Phe Thr Leu Leu Trp Ala Pro Arg Val Phe Val

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/995,225

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L:38 M:271 C: Current Filing Date differs, Replaced Current Filing Date